



#3

1

SEQUENCE LISTING

<110> BAUBET, VALERIE
LE MOUELLIC, HERVE
BRULET, PHILIPPE

<120> CHIMERIC GFP-AEQUORIN AS BIOLUMINESCENT Ca++ REPORTERS
AT THE SINGLE CELL LEVEL

<130> 03495-0207-00000

<140> 09/863,901

<141> 2001-05-24

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<151> 2000-06-01

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<151> 2000-06-06

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<160> 48

<170> PatentIn Ver. 2.1

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<213> Aequorea victoria

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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				165					170					175		
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	
			180					185					190			
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	
	195						200					205				
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	
	210					215					220					
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly	
225					230					235					240	
Leu	Arg	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	Pro	Arg	Trp	Ile	
				245					250					255		
Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	Asn	Gly	
			260					265					270			
Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	Val	Ile	
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Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	Asp	Ala	
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Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	Gly	Val	Glu	Thr	
305					310					315					320	
Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Thr	Asp	Glu	
				325					330					335		
Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	Arg	Ile	Trp	Gly	
			340					345					350			
Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	Gly	Ala	Ile	Thr	
		355					360					365				
Leu	Asp	Glu	Trp	Lys	Ala	Tyr	Thr	Lys	Ala	Ala	Gly	Ile	Ile	Gln	Ser	
	370					375					380					
Ser	Glu	Asp	Cys	Glu	Glu	Thr	Phe	Arg	Val	Cys	Asp	Ile	Asp	Glu	Ser	
385					390					395					400	
Gly	Gln	Leu	Asp	Val	Asp	Glu	Met	Thr	Arg	Gln	His	Leu	Gly	Phe	Trp	
				405					410					415		
Tyr	Thr	Met	Asp	Pro	Ala	Cys	Glu	Lys	Leu	Tyr	Gly	Gly	Ala	Val	Pro	
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 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
 225 230 235 240
 Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser Val Lys Leu Thr
 245 250 255
 Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His Lys His Met Phe
 260 265 270

Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met
 275 280 285
 Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro
 290 295 300
 Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly
 305 310 315 320
 Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu
 325 330 335
 Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn
 340 345 350
 Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val
 355 360 365
 Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr
 370 375 380
 Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr
 385 390 395 400
 Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu
 405 410 415
 Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys
 420 425 430
 Glu Lys Leu Tyr Gly Gly Ala Val Pro
 435 440

<210> 3
 <211> 450
 <212> PRT
 <213> Aequorea victoria

<400> 3
 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	100	105	110	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	115	120	125	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	130	135	140	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	145	150	155	160
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	165	170	175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	180	185	190	
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	195	200	205	
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	210	215	220	
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly	225	230	235	240
Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	245	250	255	
Ser	Gly	Leu	Arg	Ser	Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	Pro	Arg	260	265	270	
Trp	Ile	Gly	Arg	His	Lys	His	Met	Phe	Asn	Phe	Leu	Asp	Val	Asn	His	275	280	285	
Asn	Gly	Lys	Ile	Ser	Leu	Asp	Glu	Met	Val	Tyr	Lys	Ala	Ser	Asp	Ile	290	295	300	
Val	Ile	Asn	Asn	Leu	Gly	Ala	Thr	Pro	Glu	Gln	Ala	Lys	Arg	His	Lys	305	310	315	320
Asp	Ala	Val	Glu	Ala	Phe	Phe	Gly	Gly	Ala	Gly	Met	Lys	Tyr	Gly	Val	325	330	335	
Glu	Thr	Asp	Trp	Pro	Ala	Tyr	Ile	Glu	Gly	Trp	Lys	Lys	Leu	Ala	Thr	340	345	350	
Asp	Glu	Leu	Glu	Lys	Tyr	Ala	Lys	Asn	Glu	Pro	Thr	Leu	Ile	Arg	Ile	355	360	365	
Trp	Gly	Asp	Ala	Leu	Phe	Asp	Ile	Val	Asp	Lys	Asp	Gln	Asn	Gly	Ala	370	375	380	
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<213> Aequorea victoria
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			20					25					30		
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	50					55					60				
Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
65					70					75					80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105					110		
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220
 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Ser Gly
 225 230 235 240
 Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln
 245 250 255
 Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly
 260 265 270
 Gly Gln Ser Gly Leu Arg Ser Val Lys Leu Thr Ser Asp Phe Asp Asn
 275 280 285
 Pro Arg Trp Ile Gly Arg His Lys His Met Phe Asn Phe Leu Asp Val
 290 295 300
 Asn His Asn Gly Lys Ile Ser Leu Asp Glu Met Val Tyr Lys Ala Ser
 305 310 315 320
 Asp Ile Val Ile Asn Asn Leu Gly Ala Thr Pro Glu Gln Ala Lys Arg
 325 330 335
 His Lys Asp Ala Val Glu Ala Phe Phe Gly Gly Ala Gly Met Lys Tyr
 340 345 350
 Gly Val Glu Thr Asp Trp Pro Ala Tyr Ile Glu Gly Trp Lys Lys Leu
 355 360 365
 Ala Thr Asp Glu Leu Glu Lys Tyr Ala Lys Asn Glu Pro Thr Leu Ile
 370 375 380
 Arg Ile Trp Gly Asp Ala Leu Phe Asp Ile Val Asp Lys Asp Gln Asn
 385 390 395 400
 Gly Ala Ile Thr Leu Asp Glu Trp Lys Ala Tyr Thr Lys Ala Ala Gly
 405 410 415
 Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu Thr Phe Arg Val Cys Asp
 420 425 430
 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His
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 Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly
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 Gly Ala Val Pro
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<210> 5

<211> 477

<212> PRT

<213> Aequorea victoria

<400> 5

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			20					25					30		
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
	50					55					60				
Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln
65					70					75					80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105					110		
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
		195					200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly
225					230					235					240
Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln
				245					250					255	
Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly
			260					265					270		
Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Leu	Arg	Ser
		275					280					285			
Val	Lys	Leu	Thr	Ser	Asp	Phe	Asp	Asn	Pro	Arg	Trp	Ile	Gly	Arg	His
		290				295					300				

Lys His Met Phe Asn Phe Leu Asp Val Asn His Asn Gly Lys Ile Ser
 305 310 315 320
 Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Asn Asn Leu
 325 330 335
 Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala
 340 345 350
 Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro
 355 360 365
 Ala Tyr Ile Glu Gly Trp Lys Lys Leu Ala Thr Asp Glu Leu Glu Lys
 370 375 380
 Tyr Ala Lys Asn Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
 385 390 395 400
 Phe Asp Ile Val Asp Lys Asp Gln Asn Gly Ala Ile Thr Leu Asp Glu
 405 410 415
 Trp Lys Ala Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp
 420 425 430
 Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu
 435 440 445
 Asp Val Asp Glu Met Thr Arg Gln His Leu Gly Phe Trp Tyr Thr Met
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 Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro
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 <212> PRT
 <213> *Aequorea victoria*

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 Glu Gly Lys Glu Asp Ala Phe Ser Lys Leu Lys Gln Lys Phe Met Asn
 35 40 45
 Glu Leu His Lys Ile Pro Leu Pro Pro Trp Ala Leu Ile Ala Ile Ala
 50 55 60
 Ile Val Ala Val Leu Leu Val Val Thr Cys Cys Phe Cys Val Cys Lys
 65 70 75 80
 Lys Cys Leu Phe Lys Lys Lys Asn Lys Lys Lys Gly Lys Glu Lys Gly
 85 90 95

Gly	Lys	Asn	Ala	Ile	Asn	Met	Lys	Asp	Val	Lys	Asp	Leu	Gly	Lys	Thr		
			100					105					110				
Met	Lys	Asp	Gln	Ala	Leu	Lys	Asp	Asp	Asp	Ala	Glu	Thr	Gly	Leu	Thr		
		115					120					125					
Asp	Gly	Glu	Glu	Lys	Glu	Glu	Pro	Lys	Glu	Glu	Glu	Lys	Leu	Gly	Lys		
	130					135					140						
Leu	Gln	Tyr	Ser	Leu	Asp	Tyr	Asp	Phe	Gln	Asn	Asn	Gln	Leu	Leu	Val		
145					150					155					160		
Gly	Ile	Ile	Gln	Ala	Ala	Glu	Leu	Pro	Ala	Leu	Asp	Met	Gly	Gly	Thr		
			165						170						175		
Ser	Asp	Pro	Tyr	Val	Lys	Val	Phe	Leu	Leu	Pro	Asp	Lys	Lys	Lys	Lys		
			180					185					190				
Phe	Glu	Thr	Lys	Val	His	Arg	Lys	Thr	Leu	Asn	Pro	Val	Phe	Asn	Glu		
		195					200					205					
Gln	Phe	Thr	Phe	Lys	Val	Pro	Tyr	Ser	Glu	Leu	Gly	Gly	Lys	Thr	Leu		
	210					215					220						
Val	Met	Ala	Val	Tyr	Asp	Phe	Asp	Arg	Phe	Ser	Lys	His	Asp	Ile	Ile		
225					230					235					240		
Gly	Glu	Phe	Lys	Val	Pro	Met	Asn	Thr	Val	Asp	Phe	Gly	His	Val	Thr		
				245					250					255			
Glu	Glu	Trp	Arg	Asp	Leu	Gln	Ser	Ala	Glu	Lys	Glu	Glu	Gln	Glu	Lys		
			260					265					270				
Leu	Gly	Asp	Ile	Cys	Phe	Ser	Leu	Arg	Tyr	Val	Pro	Thr	Ala	Gly	Lys		
		275					280					285					
Leu	Thr	Val	Val	Ile	Leu	Glu	Ala	Lys	Asn	Leu	Lys	Lys	Met	Asp	Val		
	290					295					300						
Gly	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	Ile	His	Leu	Met	Gln	Asn	Gly		
305					310					315					320		
Lys	Arg	Leu	Lys	Lys	Lys	Lys	Thr	Thr	Ile	Lys	Lys	Asn	Thr	Leu	Asn		
				325					330					335			
Pro	Tyr	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Glu	Val	Pro	Phe	Glu	Gln	Ile		
			340					345					350				
Gln	Lys	Val	Gln	Val	Val	Val	Thr	Val	Leu	Asp	Tyr	Asp	Lys	Ile	Gly		
		355					360					365					
Lys	Asn	Asp	Ala	Ile	Gly	Lys	Val	Phe	Val	Gly	Tyr	Asn	Ser	Thr	Gly		
	370					375					380						
Ala	Glu	Leu	Arg	His	Trp	Ser	Asp	Met	Leu	Ala	Asn	Pro	Arg	Arg	Pro		
385					390					395					400		

Ile	Ala	Gln	Trp	His	Thr	Leu	Gln	Val	Glu	Glu	Glu	Val	Asp	Ala	Met			
				405					410					415				
Leu	Ala	Val	Lys	Arg	Ser	Gly	Asn	Ser	Gly	Arg	Ala	Thr	Met	Ser	Lys			
			420					425					430					
Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	Glu	Leu	Asp			
		435					440					445						
Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	Gly	Glu	Gly			
	450					455					460							
Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	Thr	Thr	Gly			
465					470					475					480			
Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	Thr	Tyr	Gly			
				485					490					495				
Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	His	Asp	Phe			
			500					505					510					
Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile	Phe			
		515					520					525						
Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	Lys	Phe	Glu			
	530					535					540							
Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	Asp	Phe	Lys			
545					550					555					560			
Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	Tyr	Asn	Ser			
			565						570					575				
His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	Ile	Lys	Ala			
			580					585					590					
Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	Gln	Leu	Ala			
		595					600					605						
Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro	Val	Leu	Leu			
	610					615					620							
Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser	Lys	Asp	Pro			
625					630					635					640			
Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val	Thr	Ala	Ala			
			645					650						655				
Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Ser	Gly	Gly	Ser	Gly			
			660					665					670					
Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly			
		675					680					685						
Ser	Gly	Ser	Gly	Gly	Gln	Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Gln	Ser			
	690					695					700							

Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser Val Lys Leu
 705 710 715 720
 Thr Ser Asp Phe Asp Asn Pro Arg Trp Ile Gly Arg His Lys His Met
 725 730 735
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 Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala Phe Phe Gly
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 Tyr Thr Lys Ala Ala Gly Ile Ile Gln Ser Ser Glu Asp Cys Glu Glu
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<213> *Aequorea victoria*

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<210> 12
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gaggacggca acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat 1740
atcatggccg acaagcagaa gaacggcatc aaggccaact tcaagatccg ccacaacatc 1800
gaggacggca gcgtgcagct cgccgaccac taccagcaga acaccccat cggcgacggc 1860
cccgtgtgct tgcccagaaa ccactacctg agcaccagc ccgccctgag caaagacccc 1920
aacgagaagc gcgatcacat ggtcctgctg aggttcgtga ccgccgcccg gatcactcac 1980
ggcatggacg agctgtacaa gtccggcggg agcggatccg gcggccagtc cggcgggagc 2040
ggatccggcg gccagtccgg cgggagcgga tccggcgccc agtccggcgg gagcggtacc 2100
ggcgccagct ccggcgggag cggatccggc ggccagtccg gcctcagatc tgtcaaactt 2160
acatcagact tcgacaaccc aagatggatt ggacgacaca agcatatgtt caatttcctt 2220
gatgtcaacc acaatggaaa aatctctctt gacgagatgg tctacaaggc atctgatatt 2280
gtcatcaata accttgagc aacacctgag caagccaaac gacacaaaga tgctgtggaa 2340
gccttcttcg gaggagctgg aatgaaatat ggtgtggaaa ctgattggcc tgcataatatt 2400
gaaggatgga aaaaattggc tactgatgaa ttggagaaat acgcaaaaaa cgaaccaacc 2460
ctcatccgca tatgggtgta tgctttgttt gatatcgctg acaaagatca aaatggagct 2520
attacactgg atgaatggaa agcatacacc aaagctgctg gtatcatcca atcatcagaa 2580
gattgcgagg aaacattcag agtgtcgcat attgatgaaa gtggacaact cgatgttgat 2640
gagatgacaa gacagcatct gggatttttg tacaccatgg atcctgcttg cgaaaagctc 2700
tacggtggag ctgtcccc 2718

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<210> 13

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of GFP-aequorin linker

<400> 13

tccggcctca gatct

15

<210> 14

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of GFP-aequorin linker

<400> 14

tccggcgggga gcggatccgg cggccagtcc ggctcagat ct

42

<210> 15

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of GFP-aequorin linker

<400> 15

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60
ctcagatct 69

<210> 16

<211> 123

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of GFP-aequorin linker

<400> 16

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcctcaga 120
tct 123

<210> 17

<211> 150

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
of GFP-aequorin linker

<400> 17

tccggcggga gcggatccgg cggccagtcc ggcgggagcg gatccggcgg ccagtccggc 60
gggagcggat ccggcggcca gtccggcggg agcggatccg gcggccagtc cggcgggagc 120
ggatccggcg gccagtccgg cctcagatct 150

<210> 18

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide
sequence of linker

<400> 18

Ser Gly Leu Arg Ser

1

5

<210> 19

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide
sequence of linker

<400> 19

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu Arg Ser
1 5 10

<210> 20

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide
sequence of linker

<400> 20

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly
1 5 10 15

Gly Gln Ser Gly Leu Arg Ser
20

<210> 21

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide
sequence of linker

<400> 21

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly
1 5 10 15

Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly
20 25 30

Ser Gly Gly Gln Ser Gly Leu Arg Ser
35 40

<210> 22

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide
sequence of linker

<400> 22

Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly
 1 5 10 15

Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly
 20 25 30

Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Leu
 35 40 45

Arg Ser
 50

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 23

ccggcgaggag cggatccggc ggccagt

27

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24

ccggactggc cgccggatcc gctcccg

27

<210> 25

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker

<220>

<223> This sequence may encompass either 9, 18, 27, 36, or 45 amino acids, with 9 or 45 amino acids being more preferable

<400> 25

Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly
 1 5 10 15

Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser Gly Gly Ser Gly Ser
 20 25 30

Gly Gly Gln Ser Gly Gly Ser Gly Ser Gly Gly Gln Ser
 35 40 45

<210> 26
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Linker

<400> 26
 Ser Gly Leu Arg Ser
 1 5

<210> 27
 <211> 27
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: pEGFP-C1 plasmid

<400> 27
 gtcgacggta ccgcgggccc gggatcc

27

<210> 28
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Illustrative
 nucleic acid

<400> 28
 gtcgacgggg atcc

14

<210> 29
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<220>
 <221> CDS
 <222> (19)..(33)

<400> 29

gcgctaccgc gggccacc atg agc aag ggc gag
 Met Ser Lys Gly Glu
 1 5

33

<210> 30

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<400> 30

Met Ser Lys Gly Glu
 1 5

<210> 31

<211> 36

<212> DNA

<213> Aequorea victoria

<220>

<221> CDS

<222> (19)..(36)

<400> 31

gcgctaccgg tcgccacc atg gtg agc aag ggc gag
 Met Val Ser Lys Gly Glu
 1 5

36

<210> 32

<211> 6

<212> PRT

<213> Aequorea victoria

<400> 32

Met Val Ser Lys Gly Glu
 1 5

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<220>

<221> CDS

<222> (3)..(20)

<400> 33
 gc atc aag gcc aac ttc aag
 Ile Lys Ala Asn Phe Lys
 1 5

20

<210> 34
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<400> 34
 Ile Lys Ala Asn Phe Lys
 1 5

<210> 35
 <211> 20
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (3) .. (20)

<400> 35
 gc atc aag gtg aac ttc aag
 Ile Lys Val Asn Phe Lys
 1 5

20

<210> 36
 <211> 6
 <212> PRT
 <213> Aequorea victoria

<400> 36
 Ile Lys Val Asn Phe Lys
 1 5

<210> 37
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<220>
 <221> CDS
 <222> (3) .. (17)

<400> 37
 gg atc act cac ggc atg ga
 Ile Thr His Gly Met
 1 5

19

<210> 38
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 construct

<400> 38
 Ile Thr His Gly Met
 1 5

<210> 39
 <211> 19
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (3)..(17)

<400> 39
 gg atc act ctc ggc atg ga
 Ile Thr Leu Gly Met
 1 5

19

<210> 40
 <211> 5
 <212> PRT
 <213> Aequorea victoria

<400> 40
 Ile Thr Leu Gly Met
 1 5

<210> 41
 <211> 596
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Altered
 Aequoria victoria sequence

<400> 41
 agcttcagat ctgtcaaact tacatcagac ttcgacaacc caagatggat tggacgacac 60
 aagcatatgt tcaatttcct tgatgtcaac cacaatggaa aaatctctct tgacgagatg 120
 gtctacaagg catctgatat tgatcatcaat aaccttggag caacacctga gcaagccaaa 180


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cgacacaaaag atgctgtgga agccttcttc ggaggagctg gaatgaaata tgggtgtggaa 240
actgattggc ctgcatatat tgaaggatgg aaaaaattgg ctactgatga attggagaaa 300
tacgccaaaa acgaaccaac cctcatccgc atctgggggtg atgctttgtt tgatatcgtt 360
gacaaagatc aaaatggagc tattacactg gatgaatgga aagcatacac caaagctgct 420
ggtatcatcc aatcatcaga agattgcgag gaaacattca gagtgtgcga tattgatgaa 480
agtggacaac tcgatgttga tgagatgaca agacagcatc tgggattttg gtacaccatg 540
gatcctgctt gcgaaaagct ctacggtgga gctgtcccct aatctcgagg atcttt 596

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<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<220>

<221> CDS

<222> (1)..(21)

<400> 42

```

aag tcc gga ctc aga tct gtc
Lys Ser Gly Leu Arg Ser Val
  1             5

```

21

<210> 43

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 43

```

Lys Ser Gly Leu Arg Ser Val
  1             5

```

<210> 44

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
construct

<400> 44

```

gacagatctg agtccggact t

```

21

<210> 45

<211> 21

<212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<400> 45
 aagtgcggac tcagatctgt c

21

<210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<400> 46
 ccggcgggag cggatccggc ggccagt

27

<210> 47
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<400> 47
 Gly Gly Ser Gly Ser Gly Gly Gln Ser
 1 5

<210> 48
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 construct

<400> 48
 ccggactggc cgccggatcc gctcccg

27